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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.40155 Seconds

(without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613B-2

Perfect score: 578  
Sequence: 1 QDWLTFQKKHKLNTKRDVDCN.....TECVICENQAPVHFVGVGHC 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	96.2	104	1	RN30_RANPI
2	292	50.5	111	1	RNP0_RANCA
3	285.5	49.4	111	1	LECS_RANCA
4	269.5	46.6	111	1	RNPL_RANCA
5	149	25.8	119	1	RNP_IGUG
6	131	22.7	124	1	RNP_IGUMU
7	130.5	22.6	145	1	ANGR_MOUSE
8	130.5	22.6	146	1	ANGI_CERAE
9	128	22.1	148	1	ANGI_BOVIN
10	126	21.8	128	1	RNP_MYOCO
11	125	21.6	124	1	RNP_BALAC
12	121.5	21.0	146	1	ANGI_MACMU
13	120	20.8	128	1	RNP_PROGU
14	119.5	20.7	145	1	ANGI_MOUSE
15	118.5	20.6	128	1	RNP_CAVPO
16	118.5	20.5	146	1	ANGI_PAPHA
17	117	20.2	124	1	RNP_CHIBR
18	116	20.1	125	1	ANGI_RABIT
19	116	20.1	128	1	RNP_HYDHY
20	114	19.7	124	1	RNP_HIPAM
21	114	19.7	146	1	ANGI_MOTFA
22	113	19.6	147	1	ANGI_HUMAN
23	113	19.6	147	1	ANGI_PANTR
24	112	19.4	124	1	RNP_PIG
25	112	19.4	150	1	RNP_BOVIN
26	112	19.4	156	1	RNP_MYOG
27	111.5	19.3	147	1	RNL4_HUMAN
28	111	19.2	128	1	RNP_HORSE
29	111	19.2	128	1	RNP_HYSCR
30	111	19.2	156	1	ECP3_MOUSE
31	111	19.2	167	1	RNBR_BOVIN
32	110.5	19.1	123	1	ANGI_PIG
33	110.5	19.1	155	1	ECPI_MOUSE

## ALIGNMENTS

34	110	19.0	141	1	RNBR_GIRCA	Q29542 giraffa cam
35	110	19.0	146	1	ANGI_SAGOE	O8w62 saguinus oe
36	110	19.0	151	1	RNBR_AXIPR	P87350 axis porcin
37	109	18.9	123	1	ANGI_BOVIN	P80929 bos taurus
38	109	18.9	124	1	RNPA_CAVPO	P00678 cavia porce
39	109	18.9	124	1	RNP_AEPME	P07847 aepyceros m
40	109	18.9	124	1	RNP_ANTAM	P00668 antilocapra
41	109	18.9	124	1	RNP_SHEEP	P00661 ovis aries
42	109	18.9	146	1	ANGI_SAIISC	O8w60 salmtr sci
43	108.5	18.8	150	1	RNKG_SAIISC	O46529 salmtr sci
44	108	18.7	124	1	RNP_BUBBU	P00657 bubalus bub
45	108	18.7	124	1	RNP_CONTA	P00660 connochaete

## RESULT 1

AC	P22069	STANDARD	PRT	104 AA.
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last annotation update)			
DE	P-30 protein (EC 3.1.27.-) (Onconase).			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Embryo;			
RX	MEDLINE=91093131; PubMed=1985896;			
RA	Ardelet W., Mikulski S.M., Shogen K.;			
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases."			
RL	J. Biol. Chem. 266:245-251(1991).			
RN	[2]			
RP	3D-STRUCTURE MODELING.			
RX	MEDLINE=93066156; PubMed=1438177;			
RA	Mosimann S.C., Johns K.L., Ardelet W., Mikulski S.M., Shogen K.;			
RT	James M.N.G.;			
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos."			
RL	Proteins 14:392-400(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RX	MEDLINE=94166079; PubMed=8120892;			
RA	Mosimann S.C., Ardelet W., James M.N.G.;			
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity."			
RL	J. Mol. Biol. 236:1141-1153(1994).			
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.			
CC	-2- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).			
CC	-3- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PDB: 1ONC; 31-JAN-94.			
DR	InterPro: IPR001427; RnaaseA.			
DR	Pfam: PF00074; RnaaseA; 1.			
DR	Prodom: PD000535; RnaaseA; 1.			
DR	SMART: SM00092; Rnaase_Pc; 1.			
DR	PROSITE: PS00127; Rnaase_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; 3d-structure.			
FT	MOD_RES			
FT	ACT_SITE			
FT	ACT_SITE			
FT	ACT_SITE			
FT	ACT_SITE			
FT	DISULFID			
FT	DISULFID			
FT	DISULFID			

FT DISULFID 87 104  
FT HELIX 3 10  
FT STRAND 11 12  
FT HELIX 19 22  
FT TURN 23 24  
FT TURN 26 30  
FT STRAND 33 38  
FT HELIX 41 48  
FT TURN 49 50  
FT STRAND 55 58  
FT STRAND 63 70  
FT TURN 74 75  
FT STRAND 77 84  
FT STRAND 86 91  
FT TURN 92 93  
FT STRAND 94 101  
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2P9E566B4 CRC64;

Query Match 96.2%; Score 556; DB 1; Length 104;  
Best Local Similarity 96.2%; Pred. No. 1e-52;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFOCKKHITNTRDYDCNNIMSTNLFHCKDKNTFIYSRPEPYKAICGIIASKNVLT 60  
D 1 QDWLTFOCKKHITNTRDYDCNNIMSTNLFHCKDKNTFIYSRPEPYKAICGIIASKNVLT 60  
QY 61 SEFYLSDCNVTSPRCCKYKIKSTNTFCVTCENAPVHFVGVC 104  
D 61 SEFYLSDCNVTSPRCCKYKIKSTNTFCVTCENAPVHFVGVC 104

RESULT 2  
RNPO\_RANCA STANDARD; PRT; 111 AA.

AC P11916;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallic acid-binding lectin) (SBL-C).  
OS Rana catesbeiana (bull. frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Egg;  
RX MEDLINE=87299649; PubMed=3304421;  
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H., Takayanagi G., Hakomori S.;  
RT "Amino acid sequence of stallic acid binding lectin from frog (Rana catesbeiana) eggs";  
RL Biochemistry 26:2189-2194(1987).  
RN [2]  
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.  
RX MEDLINE=92220613; PubMed=1373237;  
RA Liao Y.-D.;  
RT "A pyrimidine-quantum sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes";  
RL Nucleic Acids Res. 20:1371-1377(1992).  
RN [3]  
RP CHARACTERIZATION.  
RC TISSUE=Egg;  
RX MEDLINE=93192604; PubMed=8448385;  
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H., Takayanagi Y., Hakomori S., Titani K.;  
RT "Ribonuclease activity of stallic acid-binding lectin from Rana catesbeiana eggs";  
RL Glycobiology 3:37-45(1993).  
RN [4]  
RP STRUCTURE BY NMR.  
RX MEDLINE=98437383; PubMed=9761686;  
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";  
RL J. Mol. Biol. 283:231-244(1998).  
CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE RESIDUES WITH A 3'-FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C) AS SUBSTRATES, AND PREFERS THE FORMER. THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
DR PIR: A27121; A27121.  
DR PDB: 1BC4; 28-OCT-98.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; Stallic acid; Lectin; 3D-structure.  
FT MOD\_RES 1  
FT ACT\_SITE 10 10  
FT ACT\_SITE 35 35  
FT ACT\_SITE 103 103  
FT DISULFID 19 71  
FT DISULFID 34 81  
FT DISULFID 52 96  
FT DISULFID 93 110  
SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;

Query Match 50.5%; Score 292; DB 1; Length 111;  
Best Local Similarity 49.5%; Pred. No. 1.6e-24;  
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFOCKKHITNTRDYDCNNIMSTNLFHCKDKNTFIYSRPEPYKAICGIIASKNV 56  
D 1 QDWLTFOCKKHITNTRDYDCNNIMSTNLFHCKDKNTFIYSRPEPYKAICGIIASKNV 59  
QY 57 VLTSEFYLSDC---NTSPRCCKYKIKSTNTFCVTCENAPVHFVGVC 104  
D 60 VLTSEFYLSDC---NTSPRCCKYKIKSTNTFCVTCENAPVHFVGVC 110

## RESULT 3

LECS\_RANJA STANDARD; PRT; 111 AA.

AC P18839;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Stallic acid-binding lectin (EC 3.1.27.-).  
OS Rana japonica (Japanese reddish frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8402;  
RN [1]  
RP SEQUENCE, AND DISULFIDE BONDS.  
RC TISSUE=Egg;  
RX MEDLINE=91035319; PubMed=2229005;  
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K.;  
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs";  
RL J. Biochem. 108:139-143(1990).  
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR PIR: JX0120; JX0120.

[illegible]

Query Match	46.6%	Score 269.5	DB 1	Length 111
Best Local Similarity	43.2%	Pred. No. 4	1e-22	
Matches	48	Conservative	19	Mismatches 37; Indels 7; Gaps 2
QY	1	QDWLTFQKKHLTNRDVCNNIMSTNLF---	HCKDKNTFIYSRPEPKAICGIASKN	56
DB	1	QNMKFKFKHRIHRSIDTNCIMTKAIYVGCCKERTFTIISSEBDNKAICSGVSPDK	60	
QY	57	VLTISEFLISC---NTSRRCKKRLKSKTSTFCYTCENQAPVHFVYGHC	104	
DB	61	ELSTTSEKRLNCIRDSITRRCPCYPHSPDNKICVCKECKOLPVRHVGIGCK	111	
RESULT 5				
RNP_IGUG				
ID	RNP_IGUG	STANDARD:	PRT:	119 AA.
AC	P80287			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DR	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).			
OS	Iguana iguana (Common Iguana).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Iguania; Iguanidae; Iguanidae; Iguana.			
OX	NCBI_Taxid=8517;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Pancreas;			
RX	MEDLINE=94139745; PubMed=8307028;			
RA	Zhao W., Belintema J.J., Hofsteenge J.;			
RT	"The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.";			
RL	Eur. J Biochem. 219:641-646(1994).			
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: PANCREAS.			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	HSEPF, P00556; 1LSQ.			
DR	InterPro: IPR001427; RNaseA.			
DR	PIfam: PF00074; RNaseA; 1.			
DR	PRINTS: PR00794; RIBONUCLEASE.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase Pc; 1.			
DR	PROSITE, PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease.			
FT	MOD_RES	1	PYRROLIDONE CARBOXYLIC ACID.	
FT	DISULFID	25	80	BY SIMILARITY.
FT	DISULFID	39	91	BY SIMILARITY.
FT	DISULFID	57	106	BY SIMILARITY.
FT	ACT_SITE	10		BY SIMILARITY.
FT	ACT_SITE	40		BY SIMILARITY.
FT	ACT_SITE	113		BY SIMILARITY.
SO	SEQUENCE	119 AA;	13324 MW;	6072F5B7B15BD5A CRC64;
Query Match	25.8%	Score 149	DB 1	Length 119
Best Local Similarity	30.7%	Pred. No. 3	2e-09	
Matches	35	Conservative	19	Mismatches 44; Indels 16; Gaps 5
QY	1	QDWLTFQKKHL-----TNRDVCNNIM-----STNLFQCKDKNFIYSRPEPKAIC--K	49	
DB	1	QDWSEFQKHIDYDPTASNPNAVCDLMMQGRNLNPTKQCKRNTFVHASPFIQDQCSG	60	
QY	50	GIASKNVLTISE-FYLSDC-----NTSRRCKYKRLKSKTNTFCYTCENQAPVHF	98	
DB	61	GTHYEDNLNDYDSEFDLTDCKNVGCTAPSSCKYNGTPTKTRIRIACENNOAPVHF	114	
RESULT 6				
RNP_GALMU				
ID	RNP_GALMU	STANDARD:	PRT:	124 AA.

RESULT 6.	
RNP_GALMU	
ID	RNP_GALMU
STANDARD:	PRT: 124 AA.

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AC P00680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Galesa musteloides (Culis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Cavidae; Galesa.
OX NCBI_TaxID=10146;
RN [1]
RP SEQUENCE.
RX MEDLINE=87036770; PubMed=6571219;
RA Beintema J.J., Neuteboom B.;
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT of the amino acid sequences with those of two close relatives:
RT capybara and culis ribonuclease.";
RL J. Mol. Evol. 19:145-152(1983).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP; P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
DR KAT Hydrolyase; Nuclease; Endonuclease.
FT FT DISULFID 26 84 BY SIMILARITY.
FT FT DISULFID 40 95 BY SIMILARITY.
FT FT DISULFID 58 110 BY SIMILARITY.
FT FT DISULFID 65 72 BY SIMILARITY.
FT FT ACT_SITE 12 12 BY SIMILARITY.
FT FT ACT_SITE 41 41 BY SIMILARITY.
FT FT ACT_SITE 119 119 BY SIMILARITY.
FT FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ SEQUENCE 124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;

Query Match 22.7%; Score 131; DB 1; Length 124;
Best Local Similarity 30.6%; Pred. No. 2.8e-07;
Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;

OY 4 LTRPKKHL-----TNRDVCNNIM---STNLFHCKDKNTFYISREPPYKAICKGIIA 53
DB 6 MKFGRHMDSDGHDPTNTN--YCNEEMVRRSMTOGRCKPVPNTFVHEPLEAVQAVC---S 59
OY 54 SKNV-----LTTSEFYLSDCNVTSRP---CKYKLKSTNTFCVTGEN--QAPVH 97
DB 60 OKNVPCKNQGTNCYQSHSSMRTIDCRVTSSSKYFNCSTKMTQAKSITIVACEGTPSPVPH 119
OY 98 F 98
DB 120 F 120

RESULT 7
ANGL_MOUSE STANDARD; PRT; 145 AA.
AC Q64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U22519; AAA91367.1;
DR HSSP; P03950; IAAV.
DR MGD; MGI:104984; Angrp.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolase; Nuclease; Endonuclease.
FT FT CHAIN 1 24
FT FT MOD_RES 25 25
FT FT ACT_SITE 37 37 BY SIMILARITY.
FT FT ACT_SITE 64 64 BY SIMILARITY.
FT FT ACT_SITE 137 137 BY SIMILARITY.
FT FT DISULFID 50 104 BY SIMILARITY.
FT FT DISULFID 63 115 BY SIMILARITY.
FT FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;

Query Match 22.6%; Score 130.5; DB 1; Length 145;
Best Local Similarity 38.2%; Pred. No. 3.8e-07;
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

OY 30 CKDKNTFYISREPPYKAIC--KGIILAKNV--LTTSEFYLSDCNVTSR---PCKYKLKKS 82
DB 63 CKDVNTFHDTRKNKIKAIKCKGKSPYGRNLKISRSFOYTTCTYKGRSPRPPCKYRASKG 122
OY 83 TTFECVTCENQAPVHF 98
DB 123 FRILLICGECNGWPVHF 138

RESULT 8
ANGL_CERAE STANDARD; PRT; 146 AA.
AC Q8WN66;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASE5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution.";
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RL Mol. Biol. Evol. 19:438-445(2002).
CC -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOCYTELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF41664; AAL61646.1;
CC KM Hydrolase; Nuclease; Endonuclease; Angiogenesis;
CC Protein synthesis inhibitor; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 146
CC FT MOD.RES 25 25
CC FT ACT_SITE 37 37
CC FT ACT_SITE 64 64
CC FT ACT_SITE 138 138
CC FT DISULFID 50 105
CC FT DISULFID 63 116
CC FT DISULFID 81 131
CC SQ SEQUENCE 146 AA; 16444 MW; 27860112E85B8DF9 CRC64;

Query Match 22.6%; Score 130.5; DB 1; Length 146;
Best Local Similarity 30.7%; Pred. No. 3.8e-07;
Matches, 31; Conservative 17; Mismatches 30; Indels 23; Gaps 4;

Qy 5 TFGKHLTNRDVDCNNIMSTNLFHCKDKMTFTYSREPYKATC---KGIASKNV-LTT 60
Db 53 TMRNRHLTSP-----CKDITFTIGHNRHKAICGDENGNPGYENLRISK 97

Qy 61 SEFYLSDCNVT---RPCKYKLLKSTNFTVCENAPVH 97
Db 98 SPFOVTCNLRGSGSPRPCCYRATRGSRNIVGCCENCLPVH 138

RESULT 9
ANGI_BOVIN STANDARD; PRT; 148 AA.
ID ANGI_BOVIN STANDARD; PRT; 148 AA.
AC P10152; O9GKRP9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin-1 precursor (Ec 3.1.27.-).
GN ANGI OR ANG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-Liver;
RA Chang S.-I.;
RT "Cloning, sequencing, and expression of bovine angiogenin.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-148.
RC TISSUE-Milk;
RX MEDLINE=89065101; PubMed=3197838;
RA Mes P., Danart D., Rommens C., Montreuil J., Spik G., Tartar A.;
RT "The complete amino acid sequence of bovine milk angiogenin.";
```

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RL FEBS Lett. 241:41-45(1989).
RN [3]
RN SEQUENCE OF 24-148.
RC TISSUE-Plasma;
RX MEDLINE=89375344; PubMed=2775757;
RA Bond M.D., Strydom D.J.;
RT "Amino acid sequence of bovine angiogenin.";
RL Biochemistry 28:6110-6113(1989).
RN [4]
RN CHARACTERIZATION, AND SEQUENCE OF 25-55.
RC TISSUE-Plasma;
RX MEDLINE=89118214; PubMed=3064806;
RA Bond M.D., Vallee B.L.;
RT "Isolation of bovine angiogenin using a placental ribonuclease
RT inhibitor binding assay.";
RL Biochemistry 27:6282-6287(1988).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=95224057; PubMed=7708754;
RA Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
RT "Crystal structure of bovine angiogenin at 1.5-A resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
RN [6]
RN STRUCTURE BY NMR.
RX MEDLINE=96280645; PubMed=8688423;
RA Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
RT "Solution structure of bovine angiogenin by 1H nuclear magnetic
RT resonance spectroscopy.";
RL Biochemistry 35:8870-8880(1996).
RN -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
RN TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
RN ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
RN PROMOTING THE ENDOCYTELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
RN FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
RN MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
RN HYDROLYZING CELLULAR TRNAs. BINDS TIGHTLY TO PLACENTAL
RN RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
RN -1- TISSUE SPECIFICITY: SERUM, AND MILK.
RN -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
RN -----
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RN or send an email to license@isb-sib.ch).
RN -----
RN EMBL: AF135124; AAC47631.1;
RN DR PIR: A32474; A32474.
RN DR PDB: 1AGT; 03-APR-96.
RN DR PDB: 1GIO; 07-DEC-96.
RN DR InterPro: IPR001427; RNaseA.
RN DR Pfam: PF00074; RNaseA.1.
RN DR PRINTS: PR00794; RIBONUCLEASE.
RN DR Prodom: PD000535; RNaseA.1.
RN DR SMART: SM00092; RNaseA.Pc.1.
RN DR PROSITE: PS00127; RNASE_PANCREATIC.1.
RN DR Hydrolase; Nuclease; Endonuclease; Angiogenesis;
RN KW Protein synthesis inhibitor; Signal; 3D-structure.
RN FT SIGNAL 1 23
RN FT CHAIN 24 148
RN FT ACT_SITE 37 37
RN FT ACT_SITE 64 64
RN FT ACT_SITE 138 138
RN FT DISULFID 50 105
RN FT DISULFID 63 116
RN FT DISULFID 81 131
RN SQ SEQUENCE 148 AA; 16969 MW; B7999124CBB523DD CRC64;

Query Match 22.1%; Score 128; DB 1; Length 148;
Best Local Similarity 34.0%; Pred. No. 7.1e-07;
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ID	RNP_BALAC.	STANDARD:	PRT:	124 AA.
AC	p00673:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUN-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).			
NCBI	RNASL OR RNSI.			
OC	Balaenoptera aculeorostata (Minke whale) (Lesser rorqual).			
OC	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;			
OX	Balaenopteridae; Balaenoptera.			
ON	NCBI_TaxID=9767; [1]			
RP	SEQUENCE.			
RA	MEDLINE=76277855; PubMed=962870;			
RT	Emmens M., Welling G.W., Belintema J.J.:			
RL	"The amino acid sequence of pike-whale (lessor-torqual) pancreatic ribonuclease."			
CC	Biochem. J. 157:317-323(1976).			
CC	-1 CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'- phosphates and 3'-phosphooligonucleotides ending in C-p or U-p with 2',3'-cyclic phosphate intermediates.			
CC	-1 SUBCELLULAR LOCATION: Secreted.			
CC	-1 TISSUE SPECIFICITY: PANCREAS.			
CC	-1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PIR: A00818; NRMK.			
DR	HSSP: P00656; ISRN.			
DR	Interpro: IPR001427: RNaseA.			
DR	Pfam: PF00074: rnasea; 1.			
DR	PRINTS: PRO0794; RIBONUCLEASE.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATC; 1.			
KM	Hydrolase: Nuclease; Endonuclease; Glycoprotein.			
FT	DISUFLD	26	84	BY SIMILARITY.
FT	DISUFLD	40	95	BY SIMILARITY.
FT	DISUFLD	58	110	BY SIMILARITY.
FT	ACT_SITE	65	72	BY SIMILARITY.
FT	ACT_SITE	12	12	BY SIMILARITY.
FT	ACT_SITE	41	41	BY SIMILARITY.
FT	ACT_SITE	119	119	BY SIMILARITY.
FT	CARBHYD	76	76	N-LINKED (GLCNAC. .); IN 30% OF THE MOLECULES.
SQ	SEQUENCE	124 AA; 14125 MW; F57475459697E20 CRC64;		
	Query Match	21.6%; Score 125; DB 1; Length 124;		
	Best Local Similarity	28.6%; Pred. No. 1,2e-06;		
	Matches	34; Conservative	15; Mismatches	42; Indels
OY	4 LTTOKKHLLNTDVD-----CNNINSTWLF--HCKDKMTFYSREPPVKAICKGIASK	55%		
DB	6 MKFOROHHSDSGSPGNPNPCNMOMMRKRKTGCRCPVNTFFUESLEDVKAVC----	61%		
OY	56 NVV-----TTSSEFYLDSCNVSRP----CYKKLKSTNTFCVTENO--APVHF	98		
DB	62 NVLCRKGRNTCYESNSTMHITDCROTGGSKYPNCAYIKTSOKEKHIIIVACEGAPPYPVHF	120		
RESULT 12				
ANGI_MACMU				
AC	ANGI_MACMU STANDARD: PRT: 146 AA.			
OBWN63:				
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Angiogennin precursor (EC 3.1.27.-.) (Ribonuclease 5) (Rnase 5).			
GN	ANG OR RNASE5.			
OS	Maca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;			
OC	Cercopithecinae; Macaca.			
ON	NCBI_TaxID=9544; [1]			

RP SEQUENCE FROM N.A.  
 RX MEDLINE-21918422; PubMed-11919285;  
 RA Zhang J., Rosenberg H.F.;  
 RT "Diversifying selection of the tumor-growth promoter angiogenin in  
 RL primate evolution."; Mol. Biol. Evol. 19:438-445(2002).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
 CC ANGIOGENIN IS ENDOCYTOSSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF441667; AAL61649.1;  
 KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;  
 KM Protein synthesis inhibitor; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 146  
 FT MOD\_RES 25 25  
 FT ACT\_SITE 37 37  
 FT ACT\_SITE 64 64  
 FT ACT\_SITE 138 138  
 FT DISULFID 50 105  
 FT DISULFID 63 116  
 FT DISULFID 81 131  
 SQ SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;  
 Query Match 21.0%; Score 121.5; DB 1; Length 146;  
 Best Local Similarity 28.7%; Pred. No. 3.5e-06;  
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;  
 QY 5 TFOGKHLNTRDYDCNNIMSTNLFHCKDKNTFTYSRPEPKAIC--KGIISKNV-LTT 60  
 DB 53 TMRRLHUTSP-----CKDINTFVHGNNHTTALCGDENGSPYGNLRIST 97  
 QY 61 SEFYLSDCNVT-----RPCKYKLLKSTNTFCVTCEADAPVH 97  
 DB 98 SPFOVTTCKLRGSGPRPCQYRATRGSRNITVGCENGCLPVH 138  
 RESULT 13  
 RNP\_PROGU STANDARD; PRT; 128 AA.  
 AC P04059;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).  
 GN RNASE1 OR RN51.  
 OS Proechimys gualatae (Castiagua).  
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Echimyidae; Proechimys.  
 OX NCBI\_TaxID=10163;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RA MEDLINE-83000399; PubMed-7115727;  
 RA Beintema J.J., Knol G., Martena B.;  
 RT "The primary structures of pancreatic ribonucleases from African  
 RT porcupine and castiagua, two hystriocornoph rodent species."; Biochim. Biophys. Acta 705:102-110(1982).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC -----  
 DR HSP; A00821; NRKS.  
 DR HSP; P00656; ISRN.  
 DR InterPro: IPR001427; RnaseA.  
 DR Pfam: PF00794; RnaseA.1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR PRODOM: PD000535; RnaseA; 1.  
 DR SMART: SM00092; Rnase\_Pc; 1.  
 DR PROSITE: PS00127; Rnase\_PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.  
 FT DISULFID 26 84  
 FT DISULFID 40 95  
 FT DISULFID 58 110  
 FT DISULFID 65 72  
 FT ACT\_SITE 12 12  
 FT ACT\_SITE 41 41  
 FT ACT\_SITE 119 119  
 FT CARBOHYD 34 34  
 SQ SEQUENCE 128 AA; 14244 MW; 2DB58093A9D3C936 CRC64;  
 Query Match 20.8%; Score 120; DB 1; Length 128;  
 Best Local Similarity 29.9%; Pred. No. 4.3e-06;  
 Matches 35; Conservative 16; Mismatches 36; Indels 28; Gaps 7;  
 QY 6 FOKKHL-----TNRDYDCNNIM-STNLF--HCKDKNTFTYSRPEPKAICKGIISKNV 57  
 DB 8 FOKHIDSSGSPSTNPVCNAMKSRNMTGERCKPVTGPEHPLADYQAVC---FQKNV 63  
 QY 58 -----LTTSEFLSDCNVTSR---PCKYKLLKSTNTFCVTCEAD--APVHF 98  
 DB 64 PCKNGSGCYESTSNMHTDCRLTSNSKPPDCLYRTSOEKSIIIVACEGNPYVPHV 120  
 RESULT 14  
 ANGI\_MOUSE STANDARD; PRT; 145 AA.  
 ID ANGI\_MOUSE  
 AC P21570;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-).  
 GN ANG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91025023; PubMed-2222458;  
 RA Bond M.D., Vallee B.L.;  
 RT "Isolation and sequencing of mouse angiogenin DNA."; Biochem. Biophys. Res. Commun. 171:988-995(1990).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Serum;  
 RX MEDLINE-93192291; PubMed-8448182;  
 RA Bond M.D., Strydom D.J., Vallee B.L.;  
 RT "Characterization and sequencing of rabbit, pig and mouse  
 RT angiogenins: discernment of functionally important residues and  
 RT regions."; Biochim. Biophys. Acta 1162:177-186(1993).  
 RL Biochim. Biophys. Acta 1162:177-186(1993).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
 CC ANGIOGENIN IS ENDOCYTOSSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS.

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U25316; AAA91366.1; -
DR PIR: A35932; A35932.
DR HSSP: P03950; 1A4Y.
DR MGD: MGI:88022; Ang.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_PC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 145 ANGIOGENIN.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;

Query Match 20.7%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 5.6e-06;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;

QY 9 KHLNTRDQD-----CNIIMSTNLF--HCKDKMTFTYSRPEPKAIC--KGIASKN 56
DB 32 KFLQHHDAKPKGDDKRCERMKRSLTSPCKDVNTFTIHGKSNKRAICGANGSPYREN 91
OY 57 V-LTSEFYLSDCNVTST---RPCKYKLRKSTNTEFCVTCENQAPVHF 98
DB 92 LRMSKSPFYQVYTKHTGCGSPRPQCYRASAGFRHVIVACEGLPVHF 138

RESULT 15
RNPB_CAVPO STANDARD; PRT: 128 AA.
ID RNPB_CAVPO
AC P00679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=77185023; Pubmed=862624;
RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gastra W.,
RA Beintema J.;
RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT structure and glycosylation.";
RL Eur. J. Biochem. 75:91-100(1977).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
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CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
DR HSSP: P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_PC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
KW Hydrolyase; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT ACT_SITE 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT VARIANT 64 64 L -> P
SQ SEQUENCE 128 AA; 14406 MW; A2F4101A1A33E93B CRC64;

Query Match 20.6%; Score 119; DB 1; Length 128;
Best Local Similarity 28.3%; Pred. No. 5.5e-06;
Matches 34; Conservative 21; Mismatches 35; Indels 30; Gaps 7;

QY 4 LTPCKHL-----TNRDQDCNNIM---STNLFHCKDKMTFTYSRPEPKAICGIIAS 54
DB 6 MKFORQHMDEPGSPSSNSN-CNVAMLRNMTQGRKPVNTEFVESLADVOAVC---FQ 60
OY 55 KNVV-----TSEEFYLSDCNVTST---CKYKLRKSTNTEFCVTCENQ--APVHF 98
DB 61 KNVCKKNGQTCNGYSYRMRITDCRVTSSSKFRPCSTRMSQAQKSLIVACEGDPYVVF 120

Search completed: June 25, 2003, 14:50:02
Job time : 17.4016 secs
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